

[illegible]

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(iii) NUMBER OF SEQUENCES: 89

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(C) CLASSIFICATION:

(A) NAME: KULIK, David J

(B) REGISTRATION NUMBER: 36,576

(C) REFERENCE/DOCKET NUMBER: 1486/43163cp

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[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Xaa Xaa Leu His His Val Lys Leu Ile Tyr Ala Thr Xaa Xaa Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa Xaa Xaa Pro Asp Trp Xaa Xaa Arg Xaa Glu Xaa Leu Xaa Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Xaa Leu Leu His His Val Lys Leu Ile Tyr Ala Thr Lys Xaa Arg Xaa
1 5 10 15

Leu Val Gly Lys Xaa Ile Val Leu Ala Ile Pro Gly Xaa Xaa Ala Xaa
20 25 30

Xaa Xaa Xaa
35

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Xaa Xaa Xaa Pro Asp Trp Xaa Xaa Arg Xaa Glu Xaa Leu Xaa Glu Xaa
1 5 10 15

Xaa Xaa

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Xaa Tyr Asp Ala Val Ile Met Ala Ala Ala Val Val Asp Phe Arg Pro
1 5 10 15

Lys

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Asp Leu Val Val Gly Asn Thr Leu Glu Ala Phe Gly Ser Glu Glu
1 5 10 15

Asn Gln Val Val Leu Ile Gly Arg
20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Ala Met Leu His His Val Lys Leu Ile Tyr Ala Xaa Lys Leu Arg
1 5 10 15

Lys

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Ala Met Leu His His Val Lys Leu Ile Tyr Ala Thr Lys Xaa Xaa
1 5 10 15

Arg Lys

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Leu His His Val Lys Leu Ile Tyr Ala Thr Lys Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly	Xaa	Xaa	Xaa	Pro	Asp	Trp	Xaa	Xaa	Lys	Phe	Arg	Lys	Glu	Glu	Ser
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly	Ala	Ile	Leu	Leu	Pro	Asp	Trp	Lys	Ile	Arg	Lys	Glu	Ile	Leu	Ile
1				5					10					15	

Glu

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Xaa	Met	His	His	Val	Ile	Lys	Leu	Xaa	Tyr	Ala	Thr	Xaa	Ser	Arg	Lys
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Leu	Tyr	Leu	Val	Arg	Pro	Asp	Trp	Lys	Arg	Arg	Lys	Glu	Ile	Leu
1				5					10					15	

Ile Glu

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAYCAYGAHA ARYTHATTTA CGC

23

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCCATDATNA CDGCRTC GTA TTT

23

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CAYCAYGAHA ARYTHATATA CGC

23

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ARDACDACYT GRTTTTCTTC

20

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGCTTCACC	ACGTCAAGCT	AATCTACGCC	ACAAAAAGTC	GAAAGCTAGT	TGGAAAAAAG	60
ATAGTCNNNN	NNNNNCCAGG	GAGTATTGCG	GCTTTGGATG	TGAAAGCTTG	TGAGGGACTA	120
ATTAGGCATG	GGGCCGAAGT	TCATGCAGTG	ATGAGTGAGG	CAGCCACCAA	GATAATTCAT	180
CCTTATGCAT	GGAATTTGCC	CACGGGAAAT	CCAGTCATAA	CTGAGATCAC	TGGATTTATC	240
GAGCATGTTG	AGTTAGCAGG	GGAACATGAG	AATAAAGCAG	ATTTAATTTT	GGTTTGTCTT	300
GCCACTGCCA	ACACAATTAG	TAAGATTGCA	TGTGGAATAG	ATGATACTCC	AGTAACTACA	360
GTCGTGACCA	CAGCATTTC	CCACATTCCA	ATTATGATAG	CCCCAGCAAT	GCATGAGACA	420
ATGTACAGGC	ATCCCATAGT	AAGGGAGAAC	ATTGAAAGGT	TAAAGAAGCT	TGGCGTTGAG	480
TTTATAGGAC	CAAGAATTGA	GGAGGGAAAG	GCAAAGTTG	CAAGCATTGA	TGAAATAGTT	540
TACAGAGTTA	TTAAAAAGCT	CCACAAAAAA	ACATTGGAAG	GGAAGAGAGT	CCTAGTAACG	600
GCGGGAGCAA	CAAGAGAGTA	CATAGATCCA	ATAAGATTCA	TAACAAATGC	CAGCAGTGGA	660
AAAATGGGAG	TAGCGTTGGC	TGAAGAAGCA	GATTTTAGAG	GAGCTGTTAC	CCTCATAAGA	720
ACAAAGGGAA	GTGTAAAGGC	TTTLAGAATC	AGAAAAATCA	AATTGAAGGT	TGAGACAGTG	780
GAAGAAATGC	TTTCAGCGAT	TGAAAATGAG	TTGAGGAGTA	AAAAGTATGA	CGTAGTTATT	840
ATGGCAGCTG	CTGTAAGCGA	TTTLAGGCCA	AAAATTAAAG	CAGAGGGAAA	AATTAAAAGC	900
GGAAGATCAA	TAACGATAGA	GCTCGTTCCN	NNNAATCCCA	AAATCATTGA	TAGAATAAAG	960
GAAATTCAAC	CAAATGTCTT	TCTTGTGGA	TTTAAAGCAG	AACTTCAAAA	AGAAAAGCTT	1020
ATAGAAGAAG	GTAAAAGGCA	GATTGAGAGG	GCCAAGGCTG	ACTTAGTCGT	TGGTAACACA	1080
TTGGAAGCCT	TTGGAAGCGA	GGAAAACCAA	GTAGTATTAA	TTGGCAGAGA	TTTCACAAAA	1140

GAACCTTCCAA AAATGAAAAA GAGAGAGTTA GCAGAGAGAA TTTGGGATGA GATAGAGAAA 1200

TTNCTGTCC 1209

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 403 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Leu His His Val Lys Leu Ile Tyr Ala Thr Lys Ser Arg Lys Leu
1 5 10 15

Val Gly Lys Lys Ile Val Xaa Xaa Xaa Pro Gly Ser Ile Ala Ala Leu
20 25 30

Asp Val Lys Ala Cys Glu Gly Leu Ile Arg His Gly Ala Glu Val His
35 40 45

Ala Val Met Ser Glu Ala Ala Thr Lys Ile Ile His Pro Tyr Ala Trp
50 55 60

Asn Leu Pro Thr Gly Asn Pro Val Ile Thr Glu Ile Thr Gly Phe Ile
65 70 75 80

Glu His Val Glu Leu Ala Gly Glu His Glu Asn Lys Ala Asp Leu Ile
85 90 95

Leu Val Cys Pro Ala Thr Ala Asn Thr Ile Ser Lys Ile Ala Cys Gly
100 105 110

Ile Asp Asp Thr Pro Val Thr Thr Val Val Thr Thr Ala Phe Pro His
115 120 125

Ile Pro Ile Met Ile Ala Pro Ala Met His Glu Thr Met Tyr Arg His
130 135 140

Pro Ile Val Arg Glu Asn Ile Glu Arg Leu Lys Lys Leu Gly Val Glu
145 150 155 160

Phe Ile Gly Pro Arg Ile Glu Glu Gly Arg Ala Lys Val Ala Ser Ile
165 170 175

Asp Glu Ile Val Tyr Arg Val Ile Lys Lys Leu His Lys Lys Thr Leu
180 185 190

Glu Gly Lys Arg Val Leu Val Thr Ala Gly Ala Thr Arg Glu Tyr Ile

195

200

205

Asp Pro Ile Arg Phe Ile Thr Asn Ala Ser Ser Gly Lys Met Gly Val
210 215 220

Ala Leu Ala Glu Glu Ala Asp Phe Arg Gly Ala Val Thr Leu Ile Arg
225 230 235 240

Thr Lys Gly Ser Val Lys Ala Phe Arg Ile Arg Lys Ile Lys Leu Lys
245 250 255

Val Glu Thr Val Glu Glu Met Leu Ser Ala Ile Glu Asn Glu Leu Arg
260 265 270

Ser Lys Lys Tyr Asp Val Val Ile Met Ala Ala Ala Val Ser Asp Phe
275 280 285

Arg Pro Lys Ile Lys Ala Glu Gly Lys Ile Lys Ser Gly Arg Ser Ile
290 295 300

Thr Ile Glu Leu Val Pro Xaa Asn Pro Lys Ile Ile Asp Arg Ile Lys
305 310 315 320

Glu Ile Gln Pro Asn Val Phe Leu Val Gly Phe Lys Ala Glu Thr Ser
325 330 335

Lys Glu Lys Leu Ile Glu Glu Gly Lys Arg Gln Ile Glu Arg Ala Lys
340 345 350

Ala Asp Leu Val Val Gly Asn Thr Leu Glu Ala Phe Gly Ser Glu Glu
355 360 365

Asn Gln Val Val Leu Ile Gly Arg Asp Phe Thr Lys Glu Leu Pro Lys
370 375 380

Met Lys Lys Arg Glu Leu Ala Glu Arg Ile Trp Asp Glu Ile Glu Lys
385 390 395 400

Xaa Leu Ser

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATAGCGAAT TCGCAAAACC TTTCGCGGTA TGG

33

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACTACGGAAT TCCACGGAAA ATGCCGCTCA TCC

33

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGCGTTTCCG TTCTTCTTCG

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCATCTCACG CGCCAGTTTC

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAGGAGAGCA GGAAAGGTGG AAC

23

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCTGGGAGAA GACTTCACTG G

21

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAGCTTGCTC AACTTTATC

19

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GATAGAGATA GTTCTGGAG ACG

23

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGGGATATCG ACATTCTGC ACC

23

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

[illegible]

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

GAGTTAAATG CCTACACTGT ATCT

24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

CAGGACTCAG AAGCTGCTAT CGAA

24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

CTGCACGTGC CCTGTAGGAT TTGT

24

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CCAGAYTGGA ARWKNAGGAA AGA

23

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCAGAYTGGA ARWKNAGAAA AGA

23

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCAGAYTGGA ARWKNAGGAA GGA

23

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CCAGAYTGGA ARWKNAGAAA GGA

23

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAGAGTGGGC AGAGAGGCTN TTGTTAAGGG GAAATTAATC GACGTGGAAA
AGGAAGGAAA 60

AGTCGNTATT CCTCCAAGGG AATA

84

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

[illegible]

(v) FRAGMENT TYPE: internal

Glu Trp Ala Glu Arg Leu Leu Leu Arg Gly Asn Xaa Ser Lys Trp Lys
1 5 10 15

Arg Lys Glu Lys Ser Xaa Phe Leu Gln Gly Asn
20 25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: YES

(v) FRAGMENT TYPE: internal

Arg Val Gly Arg Glu Ala Xaa Val Lys Gly Lys Leu Ile Glu Val Glu
1 5 10 15

Lys Glu Gly Lys Val Xaa Ile Pro Pro Arg Glu
20 25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: YES

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Gln Ser Gly Gln Arg Gly Xaa Cys Xaa Gly Glu Ile Asn Arg Ser Gly
1 5 10 15

Lys Gly Arg Lys Ser Arg Tyr Ser Ser Lys Gly Leu
20 25

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTGCCCACTC TGAGGTCATA ACCTGCTGGT TGGAGCCATT CTCAGAAAA TGGCTCTATA 60
AGTATTTCTT TTCTGATTTT CCAGTCTGGA AGTAGCATTT TACCACCGAA ACCTTTATTT 120
TTAATTTAA 129

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Xaa Ile Lys Asn Lys Gly Phe Gly Gly Lys Met Leu Leu Pro Asp Trp
1 5 10 15

Lys Ile Arg Lys Glu Ile Leu Ile Glu Pro Phe Ser Glu Glu Trp Leu
 20 25 30

Gln Pro Ala Gly Tyr Asp Leu Arg Val Gly
 35 40

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCCTCCAAGG GAATACGCCT TAATCCTAAC CCTCGAGAGG ATAAAGTTGC CCGACGATGT	60
TATGGGGGAT ATGAAGATAA GGAGCAGTTT AGCAAGAGAA GGGGTTATTG GTTCTTTTGC	120
TTGGGTTGAC CCAGGATGGG ATGGAAACTT AACACTAATG CTCTACAATG CCTCAAATGA	180
ACCTGTCGAA TTAAGATATG GAGAGAGATT TGTGCAGATC GCATTTATAA GGCTAGAGGG	240
TCCGGCAAGA AACCCTTACA GAGGAACTA TCAGGGGAGC ACAAGGTTAG CGTTTTCAAA	300
GAGAAAGAAA CTCTAGCGTC TTTTCAATAG CATCCTCAAT ATCTCGTGTG AAGTAATCAA	360
TGTAAATACT TGCTGGGTGG GTTTTTAGGG ATTCAAATC GTAAGATGGG CCTGTATAGC	420
AGAAAACTAT TTTTGCCTCT TCTTCATTTA TCTTTCTGTG AATAAAAAAT CCAACATCCA	480
CACTAGTTCC AAAAGATATT GTTTGCGTGA TTACCAACAA GATCTTGGCA TTATTTTGA	540
TCTTATACTC TATTCTCCTT TCTCCCTCCA ATTTGCCCAA AATAAACCTG GGTAGTATAC	600
ATCACTCCT CTCTTTTAAA TTCCTATAAA TTCGTACATA GTTTAGAAAA ATGTCAAATT	660
CTTNTTCCC TGTTAAATTA ACCNCNAAAT CTTTATNANN AANCTTTTTA TAATTCCCAA	720
AACCCCTAAT TTTCCCCTTN	740

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown

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(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Leu	Gln	Gly	Asn	Thr	Pro	Xaa	Ser	Xaa	Pro	Ser	Arg	Gly	Xaa	Ser	Cys	
1				5					10					15		
Pro	Thr	Met	Leu	Trp	Gly	Ile	Xaa	Arg	Xaa	Gly	Ala	Val	Xaa	Gln	Glu	
			20				25						30			
Lys	Gly	Leu	Leu	Val	Leu	Leu	Leu	Gly	Leu	Thr	Gln	Asp	Gly	Met	Glu	
		35					40					45				
Thr	Xaa	His	Xaa	Cys	Ser	Thr	Met	Pro	Gln	Met	Asn	Leu	Ser	Asn	Xaa	
	50						55				60					
Asp	Met	Glu	Arg	Asp	Leu	Cys	Arg	Ser	His	Leu	Xaa	Gly	Xaa	Arg	Val	
65					70					75					80	
Arg	Gln	Glu	Thr	Leu	Thr	Glu	Glu	Thr	Ile	Arg	Gly	Ala	Gln	Gly	Xaa	
				85					90						95	
Arg	Phe	Gln	Arg	Glu	Arg	Asn	Ser	Ser	Val	Phe	Ser	Ile	Ala	Ser	Ser	
			100					105						110		
Ile	Ser	Arg	Val	Lys	Xaa	Ser	Met	Xaa	Ile	Leu	Ala	Gly	Trp	Val	Phe	
		115					120					125				
Arg	Asp	Ser	Asn	Ser	Xaa	Asp	Gly	Pro	Val	Xaa	Gln	Lys	Thr	Ile	Phe	
	130					135						140				
Ala	Ser	Ser	Ser	Phe	Ile	Phe	Leu	Xaa	Ile	Lys	Asn	Pro	Thr	Ser	Thr	
145					150					155					160	
Leu	Val	Pro	Lys	Asp	Ile	Val	Cys	Val	Ile	Thr	Asn	Lys	Ile	Leu	Ala	
				165					170					175		
Leu	Phe	Leu	Ile	Leu	Tyr	Ser	Ile	Leu	Leu	Ser	Pro	Ser	Asn	Leu	Pro	
			180					185						190		
Lys	Ile	Asn	Leu	Gly	Ser	Ile	His	Ser	Leu	Leu	Ser	Phe	Lys	Phe	Leu	
		195					200					205				
Xaa	Ile	Arg	Thr	Xaa	Phe	Arg	Lys	Met	Ser	Asn	Ser	Xaa	Phe	Pro	Val	
	210					215						220				

Lys Leu Thr Xaa Lys Ser Leu Xaa Xaa Xaa Phe Leu Xaa Phe Pro Lys
 225 230 235 240

Pro Leu Ile Phe Pro Xaa
 245

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Pro Pro Arg Glu Tyr Ala Leu Ile Leu Thr Leu Glu Arg Ile Lys Leu
 1 5 10 15

Pro Asn Asn Val Met Gly Asp Met Lys Ile Arg Ser Ser Leu Ala Arg
 20 25 30

Glu Gly Val Ile Gly Ser Phe Ala Trp Val Asp Pro Gly Trp Asp Gly
 35 40 45

Asn Leu Thr Leu Met Leu Tyr Asn Ala Ser Asn Glu Pro Val Glu Leu
 50 55 60

Arg Tyr Gly Glu Arg Phe Val Gln Ile Ala Phe Ile Arg Leu Glu Gly
 65 70 75 80

Pro Ala Arg Asn Pro Tyr Arg Gly Asn Tyr Gln Gly Ser Thr Arg Leu
 85 90 95

Ala Phe Ser Lys Arg Lys Lys Leu Xaa Arg Leu Phe Asn Ser Ile Leu
 100 105 110

Asn Ile Ser Cys Glu Val Ile Asn Val Asn Thr Cys Trp Val Gly Phe
 115 120 125

Xaa Gly Phe Lys Leu Val Arg Trp Ala Cys Ile Ala Glu Asn Tyr Phe
 130 135 140

Cys Leu Phe Phe Ile Tyr Leu Ser Val Asn Lys Lys Ser Asn Ile His
 145 150 155 160

Thr Ser Ser Lys Arg Tyr Cys Leu Arg Asp Tyr Gln Gln Asp Leu Gly
 165 170 175

Ile Ile Phe Asp Leu Ile Leu Tyr Ser Pro Phe Ser Leu Gln Phe Ala
 180 185 190

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Gln Asn Lys Pro Gly Xaa Tyr Thr Phe Thr Pro Leu Phe Xaa Ile Pro
 195 200 205

Ile Asn Ser Tyr Ile Val Xaa Lys Asn Val Lys Phe Phe Xaa Pro Cys
 210 215 220

Xaa Ile Asn Xaa Xaa Ile Phe Xaa Xaa Xaa Leu Phe Ile Ile Pro Lys
 225 230 235 240

Thr Pro Asn Phe Pro Leu
 245

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 246 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ser Ser Lys Gly Ile Arg Leu Asn Pro Asn Pro Arg Glu Asp Lys Val
 1 5 10 15

Ala Arg Arg Cys Tyr Gly Gly Tyr Glu Asp Lys Glu Gln Phe Ser Lys
 20 25 30

Arg Arg Gly Tyr Trp Phe Phe Cys Leu Gly Xaa Pro Arg Met Gly Trp
 35 40 45

Lys Leu Asn Thr Asn Ala Leu Gln Cys Leu Lys Xaa Thr Cys Arg Ile
 50 55 60

Lys Ile Trp Arg Glu Ile Cys Ala Asp Arg Ile Tyr Lys Ala Arg Gly
 65 70 75 80

Ser Gly Lys Lys Pro Leu Gln Arg Lys Leu Ser Gly Glu His Lys Val
 85 90 95

Ser Val Phe Lys Glu Lys Glu Thr Leu Ala Ser Phe Gln Xaa His Pro
 100 105 110

Gln Tyr Leu Val Xaa Ser Asn Gln Cys Lys Tyr Leu Leu Gly Gly Phe
 115 120 125

Leu Gly Ile Gln Thr Arg Lys Met Gly Leu Tyr Ser Arg Lys Leu Phe
 130 135 140

Leu Pro Leu Leu His Leu Ser Phe Cys Glu Xaa Lys Ile Gln His Pro
 145 150 155 160

[illegible]

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTATTGAGTA CGAACGCCAT C

21

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTCACGCTTG CTCCACTCCG

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Methanococcus Jannaschii

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Ile Ser Glu Ile Met His Pro Thr Lys Leu Leu Lys Gly Thr Lys
1 5 10 15

Ser Lys Leu Leu Glu Asn Lys Lys Ile Leu Val Ala Val Thr Ser Ser
 20 25 30

Ile Ala Ala Ile Glu Thr Pro Lys Leu Met Arg Glu Leu Ile Arg His
 35 40 45

Gly Ala Glu Val Tyr Cys Ile Ile Thr Glu Glu Thr Lys Lys Ile Ile
 50 55 60

Gly Lys Glu Ala Leu Lys Phe Gly Cys Gly Asn Glu Val Tyr Glu Glu

65				70				75				80			
Ile	Thr	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Ile	Glu	His	Ile	Leu	Leu	Tyr
				85					90					95	
Xaa	Xaa	Xaa	Xaa	Asn	Glu	Cys	Asp	Cys	Leu	Leu	Ile	Tyr	Pro	Ala	Thr
				100					105					110	
Ala	Asn	Ile	Ile	Ser	Lys	Ile	Asn	Leu	Gly	Ile	Ala	Asp	Asn	Ile	Val
				115					120					125	
Asn	Thr	Thr	Ala	Leu	Met	Phe	Phe	Gly	Asn	Lys	Pro	Ile	Phe	Ile	Val
				130					135					140	
Pro	Ala	Met	His	Glu	Asn	Met	Phe	Asn	Xaa	Xaa	Ala	Ile	Lys	Arg	His
				145					150					155	160
Ile	Asp	Lys	Leu	Lys	Glu	Lys	Asp	Lys	Ile	Tyr	Ile	Ile	Ser	Pro	Lys
				165					170					175	
Phe	Glu	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Lys	Ala	Lys	Val	Ala	Asn
				180					185					190	
Ile	Glu	Asp	Val	Val	Lys	Ala	Val	Ile	Glu	Lys	Ile	Gly	Asn	Asn	Leu
				195					200					205	
Lys	Lys	Glu	Gly	Asn	Arg	Val	Leu	Ile	Leu	Asn	Gly	Gly	Thr	Val	Glu
				210					215					220	
Phe	Ile	Asp	Lys	Val	Arg	Val	Ile	Ser	Asn	Leu	Ser	Ser	Gly	Lys	Met
				225					230					235	240
Gly	Val	Ala	Leu	Ala	Glu	Ala	Phe	Cys	Lys	Glu	Gly	Phe	Tyr	Val	Glu
				245					250					255	
Val	Ile	Thr	Ala	Met	Gly	Leu	Glu	Pro	Pro	Tyr	Tyr	Ile	Lys	Asn	His
				260					265					270	
Lys	Val	Leu	Thr	Ala	Lys	Glu	Met	Leu	Asn	Lys	Ala	Ile	Glu	Xaa	Xaa
				275					280					285	
Leu	Xaa	Ala	Lys	Asp	Phe	Asp	Ile	Ile	Ile	Ser	Ser	Ala	Ala	Ile	Ser
				290					295					300	
Asp	Phe	Thr	Val	Glu	Ser	Xaa	Phe	Glu	Gly	Lys	Leu	Ser	Ser	Glu	Glu
				305					310					315	320
Glu	Xaa	Xaa	Xaa	Xaa	Leu	Ile	Leu	Lys	Leu	Lys	Arg	Xaa	Asn	Pro	Lys
				325					330					335	
Val	Leu	Glu	Glu	Leu	Arg	Arg	Ile	Tyr	Lys	Asp	Xaa	Lys	Val	Ile	Ile
				340					345					350	
Gly	Phe	Lys	Ala	Glu	Tyr	Asn	Leu	Asp	Glu	Lys	Glu	Leu	Ile	Asn	Arg
				355					360					365	

Ala Lys Glu Arg Leu Asn Lys Tyr Asn Leu Asn Met Ile Ile Ala Asn
 370 375 380

Asp Leu Ser Lys Xaa Xaa His Tyr Phe Gly Asp Asp Tyr Ile Glu Val
 385 390 395 400

Tyr Ile Ile Thr Lys Tyr Glu Val Glu Lys Ile Ser Gly Ser Lys Lys
 405 410 415

Xaa Glu Ile Ser Glu Arg Ile Val Glu Lys Val Lys Lys Leu Val Lys
 420 425 430

Ser Xaa Xaa Xaa Xaa
 435

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Escherichia coli

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Lys Ala Arg Gln Gln Lys Tyr Cys Asp Lys Ile Ala Asn Phe Trp
 1 5 10 15

Cys His Pro Thr Gly Lys Ile Ile Met Ser Leu Ala Gly Lys Lys Ile
 20 25 30

Val Leu Gly Val Ser Gly Gly Ile Ala Ala Tyr Lys Thr Pro Glu Leu
 35 40 45

Val Arg Arg Leu Arg Asp Arg Gly Ala Asp Val Arg Val Ala Met Thr
 50 55 60

Glu Ala Ala Lys Ala Phe Ile Thr Pro Leu Ser Leu Gln Ala Val Ser
 65 70 75 80

Gly Tyr Pro Val Ser Asp Ser Leu Leu Asp Pro Ala Ala Glu Ala Ala
 85 90 95

Met Gly His Ile Glu Leu Gly Xaa Xaa Xaa Xaa Lys Trp Ala Asp Leu
 100 105 110

Val Ile Leu Ala Pro Ala Thr Ala Asp Leu Ile Ala Arg Val Ala Ala

125

Gly	Met	Ala	Asn	Asp	Leu	Val	Ser	Thr	Ile	Cys	Leu	Ala	Thr	Pro	Xaa	130	135	140
Xaa	Ala	Pro	Val	Ala	Val	Leu	Pro	Ala	Met	Asn	Gln	Gln	Met	Tyr	Arg	145	150	155
Ala	Ala	Ala	Thr	Gln	His	Asn	Leu	Glu	Val	Leu	Ala	Xaa	Ser	Arg	Gly	165	170	175
Leu	Leu	Ile	Trp	Gly	Pro	Asp	Ser	Gly	Ser	Gln	Ala	Cys	Gly	Asp	Ile	180	185	190
Gly	Pro	Gly	Arg	Xaa	Xaa	Asp	Pro	Leu	Thr	Ile	Val	Asp	Met	Ala	Val	195	200	205
Ala	His	Phe	Ser	Pro	Val	Asn	Asp	Leu	Lys	His	Leu	Asn	Ile	Met	Ile	210	215	220
Thr	Ala	Gly	Pro	Thr	Arg	Glu	Pro	Leu	Asp	Pro	Val	Arg	Tyr	Ile	Ser	225	230	235
Asn	His	Ser	Ser	Gly	Lys	Met	Gly	Phe	Ala	Ile	Ala	Ala	Ala	Ala	Ala	245	250	255
Arg	Arg	Gly	Ala	Asn	Val	Thr	Leu	Val	Ser	Gly	Pro	Val	Ser	Leu	Pro	260	265	270
Thr	Pro	Pro	Phe	Val	Lys	Arg	Val	Asp	Val	Met	Thr	Ala	Leu	Glu	Met	275	280	285
Glu	Ala	Ala	Val	Asn	Xaa	Xaa	Ala	Ser	Val	Gln	Gln	Gln	Asn	Ile	Phe	290	295	300
Ile	Gly	Cys	Ala	Ala	Val	Ala	Asp	Tyr	Arg	Ala	Ala	Thr	Val	Ala	Pro	305	310	315
Glu	Lys	Ile	Lys	Lys	Gln	Ala	Thr	Gln	Gly	Asp	Glu	Leu	Thr	Ile	Lys	325	330	335
Met	Val	Lys	Xaa	Asn	Pro	Asp	Ile	Val	Ala	Gly	Val	Ala	Ala	Leu	Lys	340	345	350
Asp	His	Arg	Pro	Tyr	Val	Val	Gly	Phe	Ala	Ala	Glu	Thr	Asn	Asn	Xaa	355	360	365
Xaa	Xaa	Xaa	Val	Glu	Glu	Tyr	Ala	Arg	Gln	Lys	Arg	Ile	Arg	Lys	Asn	370	375	380
Leu	Asp	Leu	Ile	Cys	Ala	Asn	Asp	Val	Ser	Gln	Pro	Thr	Gln	Gly	Phe	385	390	395
Asn	Ser	Asp	Asn	Asn	Ala	Leu	His	Leu	Phe	Trp	Gln	Asp	Gly	Asp	Lys	405	410	415

Val Leu Pro Leu Glu Arg Lys Glu Leu Leu Gly Gln Leu Leu Leu Asp
420 425 430

Glu Ile Val Thr Arg Tyr Asp Glu Lys Asn Arg Arg
435 440

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Xaa Gly Xaa Xaa Asp Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Phe Ala Trp Val Asp Pro Gly Trp Asp Gly Asn Thr Leu Met
1 5 10

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Gly Trp Ile Asp Ala Gly Phe Lys Gly Lys Ile Thr Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Ala Val His Asp Pro Gly Tyr Glu Gly Arg Pro Glu Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Pro Thr Ile Val Asp Ala Gly Phe Glu Gly Gln Leu Thr Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Ala His Arg Ile Asp Pro Gly Trp Ser Gly Cys Ile Val Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GAGTTAAATG CCTACACTGT ATCT

24

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CTGCACGTGC CCTGTAGGAT TTGT

24

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTATTGAGTA CGAACGCCAT C

21

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GTCACGCTTG CTCCACTCCG

20

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GAGGAGAGCA GGAAAGGTGG AAC

23

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GCTGGGAGAA GACTTCACTG G

21

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

His His Val Lys Leu Ile Tyr Ala
1 5

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Lys Tyr Asp Ala Val Ile Met Ala
1 5

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Glu Glu Asn Gln Val Val Leu
1 5

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Pro Asp Trp Lys Ile Arg Lys Glu
1 5

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGCTACTTC CAGACTGGAA AATCAGAAAA GAAATACTTA TAGAGCCATT TTCTGAAGAA	60
TCGCTCCAAC CAGCAGGTTA TGACCTCAGA GTGGGCAGAG AGGCTTTTGT TAAGGGGAAA	120
TTAATCGACG TGGAAAAGGA AGGAAAAGTC GTTATTCCTC CAAGGGAATA CGCCTTAATC	180
CTAACCCCTCG AGAGGATAAA GTTGCCCGAC GATGTTATGG GGGATATGAA GATAAGGAGC	240
AGTTTAGCAA GAGAAGGGGT TATTGGTTCT TTTGCTTGGG TTGACCCAGG ATGGGATGGA	300
AACTTAACAC TAATGCTCTA CAATGCCTCA AATGAACCTG TCGAATTAAG ATATGGAGAG	360
AGATTTGTGC AGATCGCATT TATAAGGCTA GAGGGTCCGG CAAGAAACCC TTACAGAGGA	420
AACTATCAGG GGAGCACAAG GTTAGCGTTT TCAAAGAGAA AGAAACTCTA G	471

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Leu Leu Pro Asp Trp Lys Ile Arg Lys Glu Ile Leu Ile Glu Pro
1 5 10 15
Phe Ser Glu Glu Ser Leu Gln Pro Ala Gly Tyr Asp Leu Arg Val Gly
 20 25 30
Arg Glu Ala Phe Val Lys Gly Lys Leu Ile Asp Val Glu Lys Glu Gly
 35 40 45
Lys Val Val Ile Pro Pro Arg Glu Tyr Ala Leu Ile Leu Thr Leu Glu
 50 55 60
Arg Ile Lys Leu Pro Asp Asp Val Met Gly Asp Met Lys Ile Arg Ser
65 70 75 80
Ser Leu Ala Arg Glu Gly Val Ile Gly Ser Phe Ala Trp Val Asp Pro
 85 90 95
Gly Trp Asp Gly Asn Leu Thr Leu Met Leu Tyr Asn Ala Ser Asn Glu
 100 105 110
Pro Val Glu Leu Arg Tyr Gly Glu Arg Phe Val Gln Ile Ala Phe Ile
 115 120 125
Arg Leu Glu Gly Pro Ala Arg Asn Pro Tyr Arg Gly Asn Tyr Gln Gly
 130 135 140
Ser Thr Arg Leu Ala Phe Ser Lys Arg Lys Lys Leu
145 150 155

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Xaa Gly Xaa Xaa Asp Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Phe Ala Trp Val Asp Pro Gly Trp Asp Gly Asn Thr Leu Met
1 5 10

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ala Gly Trp Ile Asp Ala Gly Phe Lys Gly Lys Ile Thr Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
0	0	1	4	9	16	25	36	49	64	81	100	121	144	169	196	225	256	289	324	361	400	441	484	529	576	625	676	729	784	841	900	961	1024	1089	1156	1225	1296	1369	1444	1521	1600	1681	1764	1849	1936	2025	2116	2209	2304	2401	2500	2601	2704	2809	2916	3025	3136	3249	3364	3481	3600	3721	3844	3969	4096	4225	4356	4489	4624	4761	4900	5041	5184	5329	5476	5625	5776	5929	6084	6241	6400	6561	6724	6889	7056	7225	7396	7569	7744	7921	8100	8281	8464	8649	8836	9025	9216	9409	9604	9801	10000

[illegible]

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
0	0	1	4	9	16	25	36	49	64	81	100	121	144	169	196	225	256	289	324	361	400	441	484	529	576	625	676	729	784	841	900	961	1024	1089	1156	1225	1296	1369	1444	1521	1600	1681	1764	1849	1936	2025	2116	2209	2304	2401	2500	2601	2704	2809	2916	3025	3136	3249	3364	3481	3600	3721	3844	3969	4096	4225	4356	4489	4624	4761	4900	5041	5184	5329	5476	5625	5776	5929	6084	6241	6400	6561	6724	6889	7056	7225	7396	7569	7744	7921	8100	8281	8464	8649	8836	9025	9216	9409	9604	9801	10000

[illegible][illegible][illegible][illegible][illegible]

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
0	0	1	4	9	16	25	36	49	64	81	100	121	144	169	196	225	256	289	324	361	400	441	484	529	576	625	676	729	784	841	900	961	1024	1089	1156	1225	1296	1369	1444	1521	1600	1681	1764	1849	1936	2025	2116	2209	2304	2401	2500	2601	2704	2809	2916	3025	3136	3249	3364	3481	3600	3721	3844	3969	4096	4225	4356	4489	4624	4761	4900	5041	5184	5329	5476	5625	5776	5929	6084	6241	6400	6561	6724	6889	7056	7225	7396	7569	7744	7921	8100	8281	8464	8649	8836	9025	9216	9409	9604	9801	10000

[illegible][illegible][illegible]

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Val	Gly	Leu	Ile	Asp	Ser	Asp	Tyr	Gln	Gly	Gln	Leu	Met	Ile
1				5					10				

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Ala	Gly	Val	Val	Asp	Arg	Asp	Tyr	Thr	Gly	Glu	Val	Lys	Val
1				5					10				

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ala Gly Val Ile Asp Glu Asp Tyr Arg Gly Asn Val Gly Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Thr Gly Leu Ile Asp Pro Gly Phe Gln Gly Glu Leu Lys Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GACGACGACA AGATGCTACT TCCAGACTGG AAA

33

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GGAACAAGAC CCGTCCCACT TTCACAGATG AAGAG

35

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GAGGAGAGCA GGAAAGGTGG AAC

23

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CTCCATGTCC CAACTCCGAT CAC

23

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GGTTTCCCA GTCACGACGT TGTAACACGA CGGCCAGT

38

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GGUUUCCCA GUCACGACGU UGUAAAACGA CGGCCAGU

38

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GACGACGACA AGATGCCCTG CTCTGAAGAG ACACC

35

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GGAACAAGAC CCGTTTAATT CTTTCCAGTG GAACC

35

CGTTTCCAGTGGAACC